

RW

PCT

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/868,605

TIME: 15:38:31

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07032001\I868605.raw

3 <110> APPLICANT: ML Laboratories PLC
 5 <120> TITLE OF INVENTION: Immunosuppression
 7 <130> FILE REFERENCE: P15700WO
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/868,605
 C--> 10 <141> CURRENT FILING DATE: 2001-06-19
 12 <150> PRIOR APPLICATION NUMBER: 9827921.9
 13 <151> PRIOR FILING DATE: 1998-12-19
 15 <150> PRIOR APPLICATION NUMBER: 9925015.1
 16 <151> PRIOR FILING DATE: 1999-10-23
 18 <160> NUMBER OF SEQ ID NOS: 39
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 288
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
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 32 20 25 30
 34 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 35 35 40 45
 37 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 38 50 55 60
 40 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 41 65 70 75 80
 43 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 44 85 90 95
 46 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 47 100 105 110
 49 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 50 115 120 125
 52 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 53 130 135 140
 55 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 56 145 150 155 160
 58 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 59 165 170 175
 61 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 62 180 185 190
 64 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
 65 195 200 205
 67 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
 68 210 215 220
 70 Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
 71 225 230 235 240
 73 Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly

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74          245          250          255
76 Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
77          260          265          270
79 Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
80          275          280          285
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87 <211> LENGTH: 972
88 <212> TYPE: DNA
89 <213> ORGANISM: Homo sapiens
91 <400> SEQUENCE: 2
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93 aagattcaag cttatttcaa tgagactgca gacctgccat gccaatgtgc aaactctcaa 120
94 aaccaaagcc tgagtgaagt agtagtattt tggcaggacc aggaaaactt ggttctgaat 180
95 gaggtatact taggcaaaga gaaatttgac agtgttcatt ccaagtatat gggccgcaca 240
96 agttttgatt cggacagttg gacctgaga cttcacaatc ttcagatcaa ggacaagggc 300
97 ttgtatcaat gtatcatcca tcacaaaaag cccacaggaa tgattcgcat ccaccagatg 360
98 aattctgaac tgtcagtgtc tgctaacttc agtcaacctg aaatagtacc aatttctaata 420
99 ataacagaaa atgtgtacat aaatttgacc tgctcatcta tacacggtta cccagaacct 480
100 aagaagatga gtgttttgct aagaaccaag aattcaacta tcgagtatga tggattatg 540
101 cagaaatctc aagataatgt cacagaactg tacgacgttt ccatcagctt gtctgtttca 600
102 ttccctgatg ttacgagcaa tatgaccatc ttctgtatc tggaaactga caagacgcgg 660
103 cttttatctt cacctttctc tatagagctt gaggaccctc agcctcccc agaccacatt 720
104 ccttgatta cagctgtact tccaacagtt attatatgtg tgatggtttt ctgtctaatt 780
105 ctatggaaat ggaagaagaa gaagcggcct cgcaactctt ataaatgtgg aaccaacaca 840
106 atggagaggg aagagagtga acagaccaag aaaagagaaa aaatccatat acctgaaaga 900
107 tctgatgaag cccagcgtgt ttttaaaagt tcgaagacat cttcatgcga caaaagtgat 960
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112 <211> LENGTH: 323
113 <212> TYPE: PRT
114 <213> ORGANISM: Homo sapiens
116 <400> SEQUENCE: 3
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120 Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
121 20 25 30
123 Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
124 35 40 45
126 Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
127 50 55 60
129 Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
130 65 70 75 80
132 Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
133 85 90 95
135 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
136 100 105 110
138 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
139 115 120 125
141 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn

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142      130      135      140
144 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
145 145      150      155      160
147 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
148      165      170      175
150 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
151      180      185      190
153 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
154      195      200      205
156 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
157      210      215      220
159 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Ile
160 225      230      235      240
162 Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys Val Met Val
163      245      250      255
165 Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Arg Pro Arg Asn
166      260      265      270
168 Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln
169      275      280      285
171 Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala
172      290      295      300
174 Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp
175 305      310      315      320
177 Thr Cys Phe
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182 <211> LENGTH: 834
183 <212> TYPE: DNA
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 4
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188 gaaccaccca ctgcatgcag agaaaaacag tacctaataa acagtcagtg ctgttctttg 120
189 tgccagccag gacagaaact ggtgagtgac tgcacagagt tcaactgaaac ggaatgcctt 180
190 ccttgcggtg aaagcgaatt cctagacacc tggaacagag agacacactg ccaccagcac 240
191 aaatactgcg accccaacct agggcttcgg gtccagcaga agggcacctc agaaacagac 300
192 accatctgca cctgtgaaga aggctggcac tgtacgagtg aggcctgtga gagctgtgtc 360
193 ctgcaccgct catgctcgcc cggctttggg gtcaagcaga ttgctacagg ggtttctgat 420
194 accatctgcg agccctgccc agtcggcttc ttctccaatg tgtcatctgc tttcgaaaaa 480
195 tgtcaccctt ggacaagctg tgagaccaa gacctggttg tgcaacaggc aggcacaaac 540
196 aagactgatg ttgtctgtgg tccccaggat cggctgagag ccctggtggt gatccccatc 600
197 atcttcggga tctgttttgc cactctcttg gtgctggtct ttatcaaaaa ggtggccaag 660
198 aagccaacca ataaggcccc ccacccaag caggaacccc aggagatcaa ttttcccagc 720
199 gatcttctcg gctccaacac tgctgtctca gtgcaggaga ctttacatgg atgccaaccg 780
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203 <210> SEQ ID NO: 5
204 <211> LENGTH: 277
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 5
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210      1          5          10          15
212 Ala Val His Pro Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu
213              20          25          30
215 Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
216              35          40          45
218 Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
219              50          55          60
221 Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His
222              65          70          75          80
224 Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
225              85          90          95
227 Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr
228              100          105          110
230 Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly
231              115          120          125
233 Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu
234              130          135          140
236 Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys
237 145          150          155          160
239 Cys His Pro Trp Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln
240              165          170          175
242 Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Leu
243              180          185          190
245 Arg Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala Ile
246              195          200          205
248 Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Thr Asn
249              210          215          220
251 Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp
252 225          230          235          240
254 Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His
255              245          250          255
257 Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser
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261              275
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265 <211> LENGTH: 735
266 <212> TYPE: PRT
267 <213> ORGANISM: Homo sapiens
269 <400> SEQUENCE: 6
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271      1          5          10          15
273 Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu Ser Arg Tyr Leu
274              20          25          30
276 Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser Thr Thr Gly Cys
277              35          40          45
279 Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp Ser Pro Leu Asn
280              50          55          60
282 Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu Thr Met Asn Pro

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283 65              70              75              80
285 Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr Ala Thr Cys Glu
286              85              90              95
288 Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile Tyr Ser Phe Pro
289              100              105              110
291 Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu Ala Gly Lys Pro
292              115              120              125
294 Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro Phe Asp Arg Leu
295              130              135              140
297 Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys Ser Gln Glu Phe
298 145              150              155              160
300 Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys Ser Leu Glu Val
301              165              170              175
303 Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val Leu Val Cys Arg
304              180              185              190
306 Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro Thr Val Arg Gln
307              195              200              205
309 Ala Val Lys Glu Leu Gln Val Tyr Ile Ser Pro Lys Asn Thr Val Ile
310              210              215              220
312 Ser Val Asn Pro Ser Thr Lys Leu Gln Glu Gly Gly Ser Val Thr Met
313 225              230              235              240
315 Thr Cys Ser Ser Glu Gly Leu Pro Ala Pro Glu Ile Phe Trp Ser Lys
316              245              250              255
318 Lys Leu Asp Asn Gly Asn Leu Gln His Leu Ser Gly Asn Ala Thr Leu
319              260              265              270
321 Thr Leu Ile Ala Met Arg Met Glu Asp Ser Gly Ile Tyr Val Cys Glu
322              275              280              285
324 Gly Val Asn Leu Ile Gly Lys Asn Arg Lys Glu Val Glu Leu Ile Val
325              290              295              300
327 Gln Glu Lys Pro Phe Thr Val Glu Ile Ser Pro Gly Pro Arg Ile Ala
328 305              310              315              320
330 Ala Gln Ile Gly Asp Ser Val Met Leu Thr Cys Ser Val Met Gly Cys
331              325              330              335
333 Glu Ser Pro Ser Phe Ser Trp Arg Thr Gln Ile Asp Ser Pro Leu Ser
334              340              345              350
336 Gly Lys Val Arg Ser Glu Gly Thr Asn Ser Thr Leu Thr Leu Ser Pro
337              355              360              365
339 Val Ser Phe Glu Asn Glu His Ser Tyr Leu Cys Thr Val Thr Cys Gly
340              370              375              380
342 His Lys Lys Leu Glu Lys Gly Ile Gln Gly Glu Leu Tyr Ser Phe Pro
343 385              390              395              400
345 Arg Asp Pro Glu Ile Glu Met Ser Gly Gly Leu Val Asn Gly Ser Ser
346              405              410              415
348 Cys Thr Val Ser Cys Lys Val Pro Ser Val Tyr Pro Leu Asp Arg Leu
349              420              425              430
351 Glu Ile Glu Leu Leu Lys Gly Glu Thr Ile Leu Glu Asn Ile Glu Phe
352              435              440              445
354 Leu Glu Asp Thr Asp Met Lys Ser Leu Glu Asn Lys Ser Leu Glu Met
355              450              455              460

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

E:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date